

SEQUENCE LISTING

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Katsutoshi, ARA
Shuji, KAWAI
Susumu, ITO

<120> GENE ENCODING ALKALINE LIQUEFYING ALPHA-AMYLASE

<130> 2173-106P

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<170> PatentIn Ver. 2.0

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<211> 1776

<212> DNA

<213> Bacillus sp.

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<221> CDS

<222> (145)..(1692)

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aaattgaagg agagggtgct tttt atg aaa ctt cat aac cgt ata att agc 171

Met Lys Leu His Asn Arg Ile Ile Ser

1

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gta cta tta aca cta ttg tta gct gta gct gtt ttg ttt cca tat atg 219

Val Leu Leu Thr Leu Leu Leu Ala Val Ala Val Leu Phe Pro Tyr Met

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25

acg gaa cca gca caa gcc cat cat aat ggg acg aat ggg acc atg atg 267

Thr Glu Pro Ala Gln Ala His His Asn Gly Thr Asn Gly Thr Met Met

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cag tat ttt gaa tgg cat ttg cca aat gac ggg aac cac tgg aac agg 315

Gln Tyr Phe Glu Trp His Leu Pro Asn Asp Gly Asn His Trp Asn Arg

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tta cga gat gac gca gct aac tta aag agt aaa ggg att acc gct gtt	363
Leu Arg Asp Asp Ala Ala Asn Leu Lys Ser Lys Gly Ile Thr Ala Val	
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tgg att cct cct gca tgg aag ggg act tcg caa aat gat gtt ggg tat	411
Trp Ile Pro Pro Ala Trp Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr	
75 80 85	
ggg gcc tat gat ttg tac gat ctt ggt gag ttt aac caa aag gga acc	459
Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr	
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gtc cgt aca aaa tat ggc aca agg agt cag ttg caa ggt gcc gtg aca	507
Val Arg Thr Lys Tyr Gly Thr Arg Ser Gln Leu Gln Gly Ala Val Thr	
110 115 120	
tct ttg aaa aat aac ggg att caa gtt tat ggg gat gtc gtg atg aat	555
Ser Leu Lys Asn Asn Gly Ile Gln Val Tyr Gly Asp Val Val Met Asn	
125 130 135	
cat aaa ggt gga gca gac ggg aca gag atg gta aat gcg gtg gaa gtg	603
His Lys Gly Gly Ala Asp Gly Thr Glu Met Val Asn Ala Val Glu Val	
140 145 150	
aac cga agc aac cga aac caa gaa ata tca ggt gaa tac acc att gaa	651
Asn Arg Ser Asn Arg Asn Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu	
155 160 165	
gca tgg acg aaa ttt gat ttc cct gga aga gga aat acc cat tcc aac	699
Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr His Ser Asn	
170 175 180 185	
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Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Gln Ser	
190 195 200	
cgt cag ctt cag aac aaa ata tat aaa ttc aga ggt acc gga aag gca	795
Arg Gln Leu Gln Asn Lys Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala	
205 210 215	
tgg gac tgg gaa gta gat ata gag aac ggc aac tat gat tac ctt atg	843
Trp Asp Trp Glu Val Asp Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met	
220 225 230	
tat gca gac att gat atg gat cat cca gaa gta atc aat gaa ctt aga	891
Tyr Ala Asp Ile Asp Met Asp His Pro Glu Val Ile Asn Glu Leu Arg	
235 240 245	

aat tgg gga gtt tgg tat aca aat aca ctt aat cta gat gga ttt aga	939
Asn Trp Gly Val Trp Tyr Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg	
250 255 260 265	
atc gat gct gtg aaa cat att aaa tac agc tat acg aga gat tgg cta	987
Ile Asp Ala Val Lys His Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu	
270 275 280	
aca cat gtg cgt aac acc aca ggt aaa cca atg ttt gca gtt gca gaa	1035
Thr His Val Arg Asn Thr Thr Gly Lys Pro Met Phe Ala Val Ala Glu	
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Phe Trp Lys Asn Asp Leu Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr	
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agt tgg aat cac tcc gtg ttc gat gtt cct ctt cat tat aat ttg tac	1131
Ser Trp Asn His Ser Val Phe Asp Val Pro Leu His Tyr Asn Leu Tyr	
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Asn Ala Ser Asn Ser Gly Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn	
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Gly Ser Val Val Gln Lys His Pro Ile His Ala Val Thr Phe Val Asp	
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Trp Phe Lys Pro Leu Ala Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly	
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Tyr Pro Ser Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly	
395 400 405	
gtt cct tcg atg aaa tct aaa att gat cca ctt ctg cag gca cgt caa	1419
Val Pro Ser Met Lys Ser Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln	
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Thr Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His His Asp Ile	
430 435 440	

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 Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser His Pro Asn Ser Gly Leu
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gca act att atg tcc gat ggg cca ggg ggt aat aaa tgg atg tat gtc 1563
 Ala Thr Ile Met Ser Asp Gly Pro Gly Gly Asn Lys Trp Met Tyr Val
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ggg aaa cat aaa gct ggc caa gta tgg aga gat atc acc gga aat agg 1611
 Gly Lys His Lys Ala Gly Gln Val Trp Arg Asp Ile Thr Gly Asn Arg
 475 480 485

tct ggt acc gtc acc att aat gca gat ggt tgg ggg aat ttc act gta 1659
 Ser Gly Thr Val Thr Ile Asn Ala Asp Gly Trp Gly Asn Phe Thr Val
 490 495 500 505

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 35 40 45
 Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala Asn
 50 55 60
 Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp Lys
 65 70 75 80
 Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp

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Arg	Ser	Gln	Leu	Gln	Gly	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly	Ile				
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Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp	Gly				
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Glu	Ile	Ser	Gly	Glu	Tyr	Thr	Ile	Glu	Ala	Trp	Thr	Lys	Phe	Asp	Phe				
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Pro	Gly	Arg	Gly	Asn	Thr	His	Ser	Asn	Phe	Lys	Trp	Arg	Trp	Tyr	His				
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Phe	Asp	Gly	Thr	Asp	Trp	Asp	Gln	Ser	Arg	Gln	Leu	Gln	Asn	Lys	Ile				
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Gly	Lys	Pro	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu	Ala				
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Tyr	Phe	Asp	Met	Arg	Asn	Ile	Leu	Asn	Gly	Ser	Val	Val	Gln	Lys	His				

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Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala Tyr		
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Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr Gly		
385	390	395 400
Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser Lys		
405	410	415
Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr Gln		
420	425	430
His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu Gly		
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Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp Gly		
450	455	460
Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly Gln		
465	470	475 480
Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile Asn		
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Trp Val Lys Gln		
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